

EXHIBIT 15

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSLVRLSLIDUYGNSPIESTDLTHALSSQFMLSISEASLNQLKSDUMLFSGLNVPFYGWLAG  
LWTWGWAKTDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHY  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPGFSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPAWTVLAYQPVLRYQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFISSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

VAGLEKDPVA

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

~~PT 7CT2~~
Muroin et al
Enfect. Imm.
61:4406, 1993



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *seq ID NO. 2*

Sequence 2 lcl|seq_2 Length 10 *PTCT2*

No significant similarity was found

BLAST 2 SEQUENCES

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☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSUVALSLIDUYGNSFYESTLUTHALSSQFALSISEASUNQKSDUDMDFSGLVNVPHTGWQJ  
LWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGPHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFT  
QGENLTSQGTFRSQTMGGAFFDLPMKPFGSTHILTAFFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
PTTSDVAGLEKDPVA
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 **SEQ ID NO: 2**

Sequence 2 lcl|seq_2 Length 15 **P27CT4**

No significant similarity was found

BLAST 2 SEQUENCES

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Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSDVLSLTIDYGNSTYESTDLTHALSSQFMLSISEASLNQLKSDUMDFSGNLNVPHYGWQV  
LWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIACQTHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCCHFYT  
QGENLTSQGTFRSQTMGGAFFDLEPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMMNATQRPQAWTVLAYQPVLRYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
PTTSDVAGLEKDPKD
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *SEQ ID NO. 2*

Sequence 2 lcl|seq_2 Length 15 *ORF 6*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

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Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSDVKLSLIDDTGNSPTSTDTLTHALSSQPMLSISEASUNQKRSDDMFSGLNVPHTGWQG  
LWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSEALTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVLRYQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
NPASTTSDVAGLEKDPVA
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *SEG ID NO. 2*

Sequence 2 lcl|seq_2 Length 18 *PTCT 7*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

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Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSUVALSLIDUYGNSFYESTDLTHALSSQFPLSISEASUNQLKSDUMDFSGLVNPHYIGWQG  
LWTWGWAKTQDPEPASSATITDPQKANRFHRTLTLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSSRHAMSYSKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
NPASTTSDVAGLEKDPKD
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequ nces results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *SEQ ID NO: 2*

Sequence 2 lcl|seq_2 Length 18 *PTFCT7*

No significant similarity was found